SEQUENCE LISTING

<110> Glaxo Wellcome PLC

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<120> Ion Channels

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<151> 1998-03-18

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<170> PatentIn Ver. 2.1

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act tcc gac tct ctg gct gcc ata aag aag cgg att gct atc caa aag     153
Thr Ser Asp Ser Leu Ala Ala Ile Lys Lys Arg Ile Ala Ile Gln Lys
 20                  25                  30                  35

gag agg aag aag tcc aaa gac aag gcg gca gct gag ccc cag cct cgg     201
Glu Arg Lys Lys Ser Lys Asp Lys Ala Ala Ala Glu Pro Gln Pro Arg
                     40                  45                  50

cct cag ctt gac cta aag gcc tcc agg aag tta cct aag ctt tat ggt     249
Pro Gln Leu Asp Leu Lys Ala Ser Arg Lys Leu Pro Lys Leu Tyr Gly
                 55                  60                  65

gac att ccc cct gag ctt gtt acg aaa cct ctg gag gac ctg gac ccc     297
Asp Ile Pro Pro Glu Leu Val Thr Lys Pro Leu Glu Asp Leu Asp Pro
                 70                  75                  80

tac tac aaa gac cat aag aca ttc atg gtg ttg aac aag aaa aga aca     345
Tyr Tyr Lys Asp His Lys Thr Phe Met Val Leu Asn Lys Lys Arg Thr
         85                  90                  95

att tat cgc ttc agc gcc aag cgg gcc ttg ttc att ctg ggg cct ttt     393
Ile Tyr Arg Phe Ser Ala Lys Arg Ala Leu Phe Ile Leu Gly Pro Phe
100                 105                 110                 115

aat ccc ctc aga agc tta atg att cgt atc tct gtc cat tca gtc ttt     441
Asn Pro Leu Arg Ser Leu Met Ile Arg Ile Ser Val His Ser Val Phe
                     120                 125                 130

agc atg ttc atc atc tgc acg gtg atc atc aac tgt atg ttc atg gcg     489
Ser Met Phe Ile Ile Cys Thr Val Ile Ile Asn Cys Met Phe Met Ala
                 135                 140                 145
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aat tct atg gag aga agt ttc gac aac gac att ccc gaa tac gtc ttc   537
Asn Ser Met Glu Arg Ser Phe Asp Asn Asp Ile Pro Glu Tyr Val Phe
         150   155   160

att ggg att tat att tta gaa gct gtg att aaa ata ttg gca aga ggc   585
Ile Gly Ile Tyr Ile Leu Glu Ala Val Ile Lys Ile Leu Ala Arg Gly
         165   170   175

ttc att gtg gat gag ttt tcc ttc ctc cga gat ccg tgg aac tgg ctg   633
Phe Ile Val Asp Glu Phe Ser Phe Leu Arg Asp Pro Trp Asn Trp Leu
180   185   190   195

gac ttc att gtc att gga aca gcg atc gca act tgt ttt ccg ggc agc   681
Asp Phe Ile Val Ile Gly Thr Ala Ile Ala Thr Cys Phe Pro Gly Ser
         200   205   210

caa gtc aat ctt tca gct ctt cgt acc ttc cga gtg ttc aga gct ctg   729
Gln Val Asn Leu Ser Ala Leu Arg Thr Phe Arg Val Phe Arg Ala Leu
         215   220   225

aag gcg att tca gtt atc tca ggt ctg aag gtc atc gta ggt gcc ctg   777
Lys Ala Ile Ser Val Ile Ser Gly Leu Lys Val Ile Val Gly Ala Leu
         230   235   240

ctg cgc tcg gtg aag aag ctg gta gac gtg atg gtc ctc act ctc ttc   825
Leu Arg Ser Val Lys Lys Leu Val Asp Val Met Val Leu Thr Leu Phe
         245   250   255

tgc ctc agc atc ttt gcc ctg gtc ggt cag cag ctg ttc atg gga att   873
Cys Leu Ser Ile Phe Ala Leu Val Gly Gln Gln Leu Phe Met Gly Ile
260   265   270   275

ctg aac cag aag tgt att aag cac aac tgt ggc ccc aac cct gca tcc   921
Leu Asn Gln Lys Cys Ile Lys His Asn Cys Gly Pro Asn Pro Ala Ser
         280   285   290

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aac aag gat tgc ttt gaa aag gaa aaa gat agc gaa gac ttc ata atg    969
Asn Lys Asp Cys Phe Glu Lys Glu Lys Asp Ser Glu Asp Phe Ile Met
        295                 300                 305


tgt ggt acc tgg ctc ggc agc aga ccc tgt ccc aat ggt tct acg tgc   1017
Cys Gly Thr Trp Leu Gly Ser Arg Pro Cys Pro Asn Gly Ser Thr Cys
        310                 315                 320


gat aaa acc aca ttg aac cca gac aat aat tat aca aag ttt gac aac   1065
Asp Lys Thr Thr Leu Asn Pro Asp Asn Asn Tyr Thr Lys Phe Asp Asn
        325                 330                 335


ttt ggc tgg tcc ttt ctc gcc atg ttc cgg gtt atg act caa gac tcc   1113
Phe Gly Trp Ser Phe Leu Ala Met Phe Arg Val Met Thr Gln Asp Ser
340                 345                 350                 355


tgg gag agg ctt tac cga cag atc ctg cgg acc tct ggg atc tac ttt   1161
Trp Glu Arg Leu Tyr Arg Gln Ile Leu Arg Thr Ser Gly Ile Tyr Phe
                360                 365                 370


gtc ttc ttc ttc gtg gtg gtc atc ttc ctg ggc tcc ttc tac ctg ctt   1209
Val Phe Phe Phe Val Val Val Ile Phe Leu Gly Ser Phe Tyr Leu Leu
                375                 380                 385


aac cta acc ctg gct gtt gtc acc atg gct tat gaa gaa cag aac aga   1257
Asn Leu Thr Leu Ala Val Val Thr Met Ala Tyr Glu Glu Gln Asn Arg
        390                 395                 400


aat gta gct gct gag aca gag gcc aag gag aaa atg ttt cag gaa gcc   1305
Asn Val Ala Ala Glu Thr Glu Ala Lys Glu Lys Met Phe Gln Glu Ala
        405                 410                 415


cag cag ctg tta agg gag gag aag gag gct ctg gtt gcc atg gga att   1353
Gln Gln Leu Leu Arg Glu Glu Lys Glu Ala Leu Val Ala Met Gly Ile
420                 425                 430                 435
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gac aga agt tcc ctt aat tcc ctt caa gct tca tcc ttt tcc ccg aag     1401
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                440             445                 450

aag agg aag ttt ttc ggt agt aag aca aga aag tcc ttc ttt atg aga     1449
Lys Arg Lys Phe Phe Gly Ser Lys Thr Arg Lys Ser Phe Phe Met Arg
                455             460                 465

ggg tcc aag acg gcc caa gcc tca gcg tct gat tca gag gac gat gcc     1497
Gly Ser Lys Thr Ala Gln Ala Ser Ala Ser Asp Ser Glu Asp Asp Ala
                470             475                 480

tct aaa aat cca cag ctc ctt gag cag acc aaa cga ctg tcc cag aac     1545
Ser Lys Asn Pro Gln Leu Leu Glu Gln Thr Lys Arg Leu Ser Gln Asn
                485             490                 495

ttg cca gtg gat ctc ttt gat gag cac gtg gac ccc ctc cac agg cag     1593
Leu Pro Val Asp Leu Phe Asp Glu His Val Asp Pro Leu His Arg Gln
500             505             510                 515

aga gcg ctg agc gct gtc agt atc tta acc atc acc ata cag gaa caa     1641
Arg Ala Leu Ser Ala Val Ser Ile Leu Thr Ile Thr Ile Gln Glu Gln
                520             525                 530

gaa aaa ttc cag gag cct tgt ttc cca tgt ggg aaa aat ttg gcc tct     1689
Glu Lys Phe Gln Glu Pro Cys Phe Pro Cys Gly Lys Asn Leu Ala Ser
                535             540                 545

aag tac ctg gtg tgg gac tgt agc cct cag tgg ctg tgc ata aag aag     1737
Lys Tyr Leu Val Trp Asp Cys Ser Pro Gln Trp Leu Cys Ile Lys Lys
                550             555             560

gtc ctg cgg acc atc atg acg gat ccc ttt act gag ctg gcc atc acc     1785
Val Leu Arg Thr Ile Met Thr Asp Pro Phe Thr Glu Leu Ala Ile Thr
                565             570             575
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atc tgc atc atc atc aat acc gtt ttc tta gcc gtg gag cac cac aac   1833
Ile Cys Ile Ile Ile Asn Thr Val Phe Leu Ala Val Glu His His Asn
580   585   590   595

atg gat gac aac tta aag acc ata ctg aaa ata gga aac tgg gtt ttc   1881
Met Asp Asp Asn Leu Lys Thr Ile Leu Lys Ile Gly Asn Trp Val Phe
             600   605   610

acg gga att ttc ata gcg gaa atg tgt ctc aag atc atc gcg ctc gac   1929
Thr Gly Ile Phe Ile Ala Glu Met Cys Leu Lys Ile Ile Ala Leu Asp
             615   620   625

cct tac cac tac ttc cgg cac ggc tgg aat gtt ttt gac agc atc gtg   1977
Pro Tyr His Tyr Phe Arg His Gly Trp Asn Val Phe Asp Ser Ile Val
            630   635   640

gcc ctc ctg agt ctc gct gat gtg ctc tac aac aca ctg tct gat aac   2025
Ala Leu Leu Ser Leu Ala Asp Val Leu Tyr Asn Thr Leu Ser Asp Asn
             645   650   655

aat agg tct ttc ttg gct tcc ctc aga gtg ctg agg gtc ttc aag tta   2073
Asn Arg Ser Phe Leu Ala Ser Leu Arg Val Leu Arg Val Phe Lys Leu
660   665   670   675

gcc aaa tcc tgg ccc acg tta aac act ctc att aag atc atc ggc cac   2121
Ala Lys Ser Trp Pro Thr Leu Asn Thr Leu Ile Lys Ile Ile Gly His
             680   685   690

tcc gtg ggc gcg ctt gga aac ctg act gtg gtc ctg act atc gtg gtc   2169
Ser Val Gly Ala Leu Gly Asn Leu Thr Val Val Leu Thr Ile Val Val
             695   700   705

ttc atc ttt tct gtg gtg ggc atg cgg ctc ttc ggc acc aag ttt aac   2217
Phe Ile Phe Ser Val Val Gly Met Arg Leu Phe Gly Thr Lys Phe Asn
             710   715   720

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Lys Thr Ala Tyr Ala Thr Gln Glu Arg Pro Arg Arg Arg Trp His Met
        725                 730                 735

gat aat ttc tac cac tcc ttc ctg gtg gtg ttc cgc atc ctc tgt ggg     2313
Asp Asn Phe Tyr His Ser Phe Leu Val Val Phe Arg Ile Leu Cys Gly
740                 745                 750                 755

gaa tgg atc gag aac atg tgg ggc tgc atg cag gat atg gac ggc tcc     2361
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                    760                 765                 770

ccg ttg tgc atc att gtc ttt gtc ctg ata atg gtg atc ggg aag ctt     2409
Pro Leu Cys Ile Ile Val Phe Val Leu Ile Met Val Ile Gly Lys Leu
            775                 780                 785

gtg gtg ctt aac ctc ttc att gcc ttg ctg ctc aat tcc ttc agc aat     2457
Val Val Leu Asn Leu Phe Ile Ala Leu Leu Leu Asn Ser Phe Ser Asn
            790                 795                 800

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Glu Glu Lys Asp Gly Ser Leu Glu Gly Glu Thr Arg Lys Thr Lys Val
        805                 810                 815

cag cta gcc ctg gat cgg ttc cgc cgg gcc ttc tcc ttc atg ctg cac     2553
Gln Leu Ala Leu Asp Arg Phe Arg Arg Ala Phe Ser Phe Met Leu His
820                 825                 830                 835

gct ctt cag agt ttt tgt tgc aag aaa tgc agg agg aaa aac tcg cca     2601
Ala Leu Gln Ser Phe Cys Cys Lys Lys Cys Arg Arg Lys Asn Ser Pro
                    840                 845                 850

aag cca aaa gag aca aca gaa agc ttt gct ggt gag aat aaa gac tca     2649
Lys Pro Lys Glu Thr Thr Glu Ser Phe Ala Gly Glu Asn Lys Asp Ser
                855                 860                 865
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atc ctc ccg gat gcg agg ccc tgg aag gag tat gat aca gac atg gct    2697
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        870             875             880


ttg tac act gga cag gcc ggg gct ccg ctg gcc cca ctc gca gag gta    2745
Leu Tyr Thr Gly Gln Ala Gly Ala Pro Leu Ala Pro Leu Ala Glu Val
        885             890             895


gag gac gat gtg gaa tat tgt ggt gaa ggc ggt gcc cta ccc acc tca    2793
Glu Asp Asp Val Glu Tyr Cys Gly Glu Gly Gly Ala Leu Pro Thr Ser
900             905             910             915


caa cat agt gct gga gtt cag gcc ggt gac ctc cct cca gag acc aag    2841
Gln His Ser Ala Gly Val Gln Ala Gly Asp Leu Pro Pro Glu Thr Lys
            920             925             930


cag ctc act agc ccg gat gac caa ggg gtt gaa atg gaa gta ttt tct    2889
Gln Leu Thr Ser Pro Asp Asp Gln Gly Val Glu Met Glu Val Phe Ser
        935             940             945


gaa gaa gat ctg cat tta agc ata cag agt cct cga aag aag tct gac    2937
Glu Glu Asp Leu His Leu Ser Ile Gln Ser Pro Arg Lys Lys Ser Asp
        950             955             960


gca gtg agc atg ctc tcg gaa tgc agc aca att gac ctg aat gat atc    2985
Ala Val Ser Met Leu Ser Glu Cys Ser Thr Ile Asp Leu Asn Asp Ile
        965             970             975


ttt aga aat tta cag aaa aca gtt tcc ccc aaa aag cag cca gat aga    3033
Phe Arg Asn Leu Gln Lys Thr Val Ser Pro Lys Lys Gln Pro Asp Arg
980             985             990             995


tgc ttt ccc aag ggc ctt agt tgt cac ttt cta tgc cac aaa aca gac    3081
Cys Phe Pro Lys Gly Leu Ser Cys His Phe Leu Cys His Lys Thr Asp
            1000            1005            1010
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aag aga aag tcc ccc tgg gtc ctg tgg tgg aac att cgg aaa acc tgc   3129
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tac caa atc gtg aag cac agc tgg ttt gag agt ttc ata atc ttt gtt   3177
Tyr Gln Ile Val Lys His Ser Trp Phe Glu Ser Phe Ile Ile Phe Val
            1030   1035   1040

att ctg ctg agc agt gga gcg ctg ata ttt gaa gat gtc aat ctc ccc   3225
Ile Leu Leu Ser Ser Gly Ala Leu Ile Phe Glu Asp Val Asn Leu Pro
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agc cgg ccc caa gtt gag aaa tta cta agg tgt acc gat aat att ttc   3273
Ser Arg Pro Gln Val Glu Lys Leu Leu Arg Cys Thr Asp Asn Ile Phe
1060   1065   1070   1075

aca ttt att ttc ctc ctg gaa atg atc ctg aag tgg gtg gcc ttt gga   3321
Thr Phe Ile Phe Leu Leu Glu Met Ile Leu Lys Trp Val Ala Phe Gly
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ttc cgg agg tat ttc acc agt gcc tgg tgc tgg ctt gat ttc ctc att   3369
Phe Arg Arg Tyr Phe Thr Ser Ala Trp Cys Trp Leu Asp Phe Leu Ile
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gtg gtg gtg tct gtg ctc agt ctc atg aat cta cca agc ttg aag tcc   3417
Val Val Val Ser Val Leu Ser Leu Met Asn Leu Pro Ser Leu Lys Ser
            1110   1115   1120

ttc cgg act ctg cgg gcc ctg aga cct ctg cgg gcg ctg tcc cag ttt   3465
Phe Arg Thr Leu Arg Ala Leu Arg Pro Leu Arg Ala Leu Ser Gln Phe
         1125   1130   1135

gaa gga atg aag gtt gtc gtc tac gcc ctg atc agc gcc ata cct gcc   3513
Glu Gly Met Lys Val Val Val Tyr Ala Leu Ile Ser Ala Ile Pro Ala
1140   1145   1150   1155

att ctc aat gtc ttg ctg gtc tgc ctc att ttc tgg ctc gta ttt tgt   3561
Ile Leu Asn Val Leu Leu Val Cys Leu Ile Phe Trp Leu Val Phe Cys
           1160   1165   1170

atc ttg gga gta aat tta ttt tct ggg aag ttt gga agg tgc att aac   3609
Ile Leu Gly Val Asn Leu Phe Ser Gly Lys Phe Gly Arg Cys Ile Asn
           1175   1180   1185

ggg aca gac ata aat atg tat ttg gat ttt acc gaa gtt ccg aac cga   3657
Gly Thr Asp Ile Asn Met Tyr Leu Asp Phe Thr Glu Val Pro Asn Arg
           1190   1195   1200

agc caa tgt aac att agt aat tac tcg tgg aag gtc ccg cag gtc aac   3705
Ser Gln Cys Asn Ile Ser Asn Tyr Ser Trp Lys Val Pro Gln Val Asn
     1205   1210   1215

ttt gac aac gtg ggg aat gcc tat ctc gcc ctg ctg caa gtg gca acc   3753
Phe Asp Asn Val Gly Asn Ala Tyr Leu Ala Leu Leu Gln Val Ala Thr
1220   1225   1230   1235

tat aag ggc tgg ctg gaa atc atg aat gct gct gtc gat tcc aga gag   3801
Tyr Lys Gly Trp Leu Glu Ile Met Asn Ala Ala Val Asp Ser Arg Glu
           1240   1245   1250

aaa gac gag cag ccg gac ttt gag gcg aac ctc tac gcg tat ctc tac   3849
Lys Asp Glu Gln Pro Asp Phe Glu Ala Asn Leu Tyr Ala Tyr Leu Tyr
           1255   1260   1265

ttt gtg gtt ttt atc atc ttc ggc tcc ttc ttt acc ctg aac ctc ttt   3897
Phe Val Val Phe Ile Ile Phe Gly Ser Phe Phe Thr Leu Asn Leu Phe
           1270   1275   1280

atc ggt gtt att att gac aac ttc aat cag cag cag aaa aag tta ggt   3945
Ile Gly Val Ile Ile Asp Asn Phe Asn Gln Gln Gln Lys Lys Leu Gly
     1285   1290   1295

ggc caa gac att t t atg aca gaa gaa cag aag aaa tat tac aat gca   3993
Gly Gln Asp Ile Phe Met Thr Glu Glu Gln Lys Lys Tyr Tyr Asn Ala
1300   1305   1310   1315

atg aaa aag tta gga acc aag aaa cct caa aag ccc atc cca agg ccc   4041
Met Lys Lys Leu Gly Thr Lys Lys Pro Gln Lys Pro Ile Pro Arg Pro
           1320   1325   1330

ctg aac aaa tgt caa gcc ttt gtg ttc gac ctg gtc aca agc cag gtc   4089
Leu Asn Lys Cys Gln Ala Phe Val Phe Asp Leu Val Thr Ser Gln Val
      1335   1340   1345

ttt gac gtc atc att ctg ggt ctt att gtc tta aat atg att atc atg   4137
Phe Asp Val Ile Ile Leu Gly Leu Ile Val Leu Asn Met Ile Ile Met
     1350   1355   1360

atg gct gaa tct gcc gac cag ccc aaa gat gtg aag aaa acc ttt gat   4185
Met Ala Glu Ser Ala Asp Gln Pro Lys Asp Val Lys Lys Thr Phe Asp
   1365   1370   1375

atc ctc aac ata gcc ttc gtg gtc atc ttt acc ata gag tgt ctc atc   4233
Ile Leu Asn Ile Ala Phe Val Val Ile Phe Thr Ile Glu Cys Leu Ile
1380   1385   1390   1395

aaa gtc ttt gct ttg agg caa cac tac ttc acc aat ggc tgg aac tta   4281
Lys Val Phe Ala Leu Arg Gln His Tyr Phe Thr Asn Gly Trp Asn Leu
           1400   1405   1410

ttt gat tgt gtg gtc gtg gtt ctt tct atc att agt acc ctg gtt tcc   4329
Phe Asp Cys Val Val Val Val Leu Ser Ile Ile Ser Thr Leu Val Ser
       1415   1420   1425

cgc ttg gag gac agt gac att tct ttc ccg ccc acg ctc ttc aga gtc   4377
Arg Leu Glu Asp Ser Asp Ile Ser Phe Pro Pro Thr Leu Phe Arg Val
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gtc cgc ttg gct cgg att ggt cga atc ctc agg ctg gtc cgg gct gcc   4425
Val Arg Leu Ala Arg Ile Gly Arg Ile Leu Arg Leu Val Arg Ala Ala
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cgg gga atc agg acc ctc ctc ttt gct ttg atg atg tct ctc ccc tct   4473
Arg Gly Ile Arg Thr Leu Leu Phe Ala Leu Met Met Ser Leu Pro Ser
1460   1465   1470   1475

ctc ttc aac atc ggt ctg ctg ctc ttc ctg gtg atg ttc att tac gcc   4521
Leu Phe Asn Ile Gly Leu Leu Leu Phe Leu Val Met Phe Ile Tyr Ala
           1480   1485   1490

atc ttt ggg atg agc tgg ttt tcc aaa gtg aag aag ggc tcc ggg atc   4569
Ile Phe Gly Met Ser Trp Phe Ser Lys Val Lys Lys Gly Ser Gly Ile
           1495   1500   1505

gac gac atc ttc aac ttc gag acc ttt acg ggc agc atg ctg tgc ctc   4617
Asp Asp Ile Phe Asn Phe Glu Thr Phe Thr Gly Ser Met Leu Cys Leu
           1510   1515   1520

ttc cag ata acc act tcg gct ggc tgg gat acc ctc ctc aac ccc atg   4665
Phe Gln Ile Thr Thr Ser Ala Gly Trp Asp Thr Leu Leu Asn Pro Met
    1525   1530   1535

ctg gag gca aaa gaa cac tgc aac tcc tcc tcc caa gac agc tgt cag   4713
Leu Glu Ala Lys Glu His Cys Asn Ser Ser Ser Gln Asp Ser Cys Gln
1540   1545   1550   1555

cag ccg cag ata gcc gtc gtc tac ttc gtc agt tac atc atc atc tcc   4761
Gln Pro Gln Ile Ala Val Val Tyr Phe Val Ser Tyr Ile Ile Ile Ser
           1560   1565   1570

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gaa atc ttc tat gag gtc tgg gag aag ttt gac ccc gag gcg tcg cag      4905
Glu Ile Phe Tyr Glu Val Trp Glu Lys Phe Asp Pro Glu Ala Ser Gln
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Phe Ile Gln Tyr Ser Ala Leu Ser Asp Phe Ala Asp Ala Leu Pro Glu
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Pro Leu Arg Val Ala Lys Pro Asn Lys Phe Gln Phe Leu Val Met Asp
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ttg ccc atg gtg atg ggc gac cgc ctc cat tgc atg gat gtt ctc ttt      5049
Leu Pro Met Val Met Gly Asp Arg Leu His Cys Met Asp Val Leu Phe
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gct ttc act acc agg gtc ctc ggg gac tcc agc ggc ttg gat acc atg      5097
Ala Phe Thr Thr Arg Val Leu Gly Asp Ser Ser Gly Leu Asp Thr Met
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Gly Ala Ala Val Ile Gln Arg Ala Tyr Arg Lys His Met Glu Lys Met
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gtc aaa ctg agg ctg aag gac agg tca agt tca tcg cac cag gtg ttt   5289
Val Lys Leu Arg Leu Lys Asp Arg Ser Ser Ser Ser His Gln Val Phe
         1735   1740   1745

tgc aat gga gac ttg tcc agc ttg gat gtg gcc aag gtc aag gtt cac   5337
Cys Asn Gly Asp Leu Ser Ser Leu Asp Val Ala Lys Val Lys Val His
         1750   1755   1760

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Asn Asp
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Arg Pro Phe Thr Ser Asp Ser Leu Ala Ala Ile Lys Lys Arg Ile Ala
           20   25   30

Ile Gln Lys Glu Arg Lys Lys Ser Lys Asp Lys Ala Ala Ala Glu Pro
           35   40   45

Gln Pro Arg Pro Gln Leu Asp Leu Lys Ala Ser Arg Lys Leu Pro Lys
           50 -   55   60

Leu Tyr Gly Asp Ile Pro Pro Glu Leu Val Thr Lys Pro Leu Glu Asp
65   70   75   80

Leu Asp Pro Tyr Tyr Lys Asp His Lys Thr Phe Met Val Leu Asn Lys
                       85   90   95

Lys Arg Thr Ile Tyr Arg Phe Ser Ala Lys Arg Ala Leu Phe Ile Leu
                       100   105   110

Gly Pro Phe Asn Pro Leu Arg Ser Leu Met Ile Arg Ile Ser Val His
           115   120   125

Ser Val Phe Ser Met Phe Ile Ile Cys Thr Val Ile Ile Asn Cys Met
           130   135   140

Phe Met Ala Asn Ser Met Glu Arg Ser Phe Asp Asn Asp Ile Pro Glu
145   150   155   160

Tyr Val Phe Ile Gly Ile Tyr Ile Leu Glu Ala Val Ile Lys Ile Leu
                       165   170   175

Ala Arg Gly Phe Ile Val Asp Glu Phe Ser Phe Leu Arg Asp Pro Trp
                       180   185   190

Asn Trp Leu Asp Phe Ile Val Ile Gly Thr Ala Ile Ala Thr Cys Phe
      195   200   205

Pro Gly Ser Gln Val Asn Leu Ser Ala Leu Arg Thr Phe Arg Val Phe
      210   215   220

Arg Ala Leu Lys Ala Ile Ser Val Ile Ser Gly Leu Lys Val Ile Val
225   230   235   240

Gly Ala Leu Leu Arg Ser Val Lys Lys Leu Val Asp Val Met Val Leu
            245   250   255

Thr Leu Phe Cys Leu Ser Ile Phe Ala Leu Val Gly Gln Gln Leu Phe
      260   265   270

Met Gly Ile Leu Asn Gln Lys Cys Ile Lys His Asn Cys Gly Pro Asn
      275   280   285

Pro Ala Ser Asn Lys Asp Cys Phe Glu Lys Glu Lys Asp Ser Glu Asp
      290   295   300

Phe Ile Met Cys Gly Thr Trp Leu Gly Ser Arg Pro Cys Pro Asn Gly
305   310   315   320

Ser Thr Cys Asp Lys Thr Thr Leu Asn Pro Asp Asn Asn Tyr Thr Lys
            325   330   335

Phe Asp Asn Phe Gly Trp Ser Phe Leu Ala Met Phe Arg Val Met Thr
            340   345   350

Gln Asp Ser Trp Glu Arg Leu Tyr Arg Gln Ile Leu Arg Thr Ser Gly
      355   360   365

Ile Tyr Phe Val Phe Phe Phe Val Val Val Ile Phe Leu Gly Ser Phe
      370   375   380

Tyr Leu Leu Asn Leu Thr Leu Ala Val Val Thr Met Ala Tyr Glu Glu

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385                    390                   395                   400
Gln Asn Arg Asn Val Ala Ala Glu Thr Glu Ala Lys Glu Lys Met Phe
                    405           ·             410               415


Gln Glu Ala Gln Gln Leu Leu Arg Glu Glu Lys Glu Ala Leu Val Ala
                420                   425                   430


Met Gly Ile Asp Arg Ser Ser Leu Asn Ser Leu Gln Ala Ser Ser Phe
            435               440               445


Ser Pro Lys Lys Arg Lys Phe Phe Gly Ser Lys Thr Arg Lys Ser Phe
        450               455               460


Phe Met Arg Gly Ser Lys Thr Ala Gln Ala Ser Ala Ser Asp Ser Glu
465               470               475                   480


Asp Asp Ala Ser Lys Asn Pro Gln Leu Leu Glu Gln Thr Lys Arg Leu
                485               490               495


Ser Gln Asn Leu Pro Val Asp Leu Phe Asp Glu His Val Asp Pro Leu
            500               505               510


His Arg Gln Arg Ala Leu Ser Ala Val Ser Ile Leu Thr Ile Thr Ile
            515               520               525


Gln Glu Gln Glu Lys Phe Gln Glu Pro Cys Phe Pro Cys Gly Lys Asn
        530               535               540


Leu Ala Ser Lys Tyr Leu Val Trp Asp Cys Ser Pro Gln Trp Leu Cys
545               550               555               560


Ile Lys Lys Val Leu Arg Thr Ile Met Thr Asp Pro Phe Thr Glu Leu
                565               570               575


Ala Ile Thr Ile Cys Ile Ile Ile Asn Thr Val Phe Leu Ala Val Glu
            580               585               590
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His His Asn Met Asp Asp Asn Leu Lys Thr Ile Leu Lys Ile Gly Asn
    595   600   605

Trp Val Phe Thr Gly Ile Phe Ile Ala Glu Met Cys Leu Lys Ile Ile
    610   615   620

Ala Leu Asp Pro Tyr His Tyr Phe Arg His Gly Trp Asn Val Phe Asp
625   630   635   640

Ser Ile Val Ala Leu Leu Ser Leu Ala Asp Val Leu Tyr Asn Thr Leu
        645   650   655

Ser Asp Asn Asn Arg Ser Phe Leu Ala Ser Leu Arg Val Leu Arg Val
        660   665   670

Phe Lys Leu Ala Lys Ser Trp Pro Thr Leu Asn Thr Leu Ile Lys Ile
        675   680   685

Ile Gly His Ser Val Gly Ala Leu Gly Asn Leu Thr Val Val Leu Thr
        690   695   700

Ile Val Val Phe Ile Phe Ser Val Val Gly Met Arg Leu Phe Gly Thr
705   710   715   720

Lys Phe Asn Lys Thr Ala Tyr Ala Thr Gln Glu Arg Pro Arg Arg Arg
        725   730   735

Trp His Met Asp Asn Phe Tyr His Ser Phe Leu Val Val Phe Arg Ile
        740   745   750

Leu Cys Gly Glu Trp Ile Glu Asn Met Trp Gly Cys Met Gln Asp Met
        755   760   765

Asp Gly Ser Pro Leu Cys Ile Ile Val Phe Val Leu Ile Met Val Ile
        770   775   780

Gly Lys Leu Val Val Leu Asn Leu Phe Ile Ala Leu Leu Leu Asn Ser
785   790   795   800

Phe Ser Asn Glu Glu Lys Asp Gly Ser Leu Glu Gly Glu Thr Arg Lys
            805   810   815

Thr Lys Val Gln Leu Ala Leu Asp Arg Phe Arg Arg Ala Phe Ser Phe
         820   825   830

Met Leu His Ala Leu Gln Ser Phe Cys Cys Lys Lys Cys Arg Arg Lys
         835   840   845

Asn Ser Pro Lys Pro Lys Glu Thr Thr Glu Ser Phe Ala Gly Glu Asn
         850   855   860

Lys Asp Ser Ile Leu Pro Asp Ala Arg Pro Trp Lys Glu Tyr Asp Thr
865   870   875   880

Asp Met Ala Leu Tyr Thr Gly Gln Ala Gly Ala Pro Leu Ala Pro Leu
         885   890   895

Ala Glu Val Glu Asp Asp Val Glu Tyr Cys Gly Glu Gly Gly Ala Leu
         900   905   910

Pro Thr Ser Gln His Ser Ala Gly Val Gln Ala Gly Asp Leu Pro Pro
         915   920   925

Glu Thr Lys Gln Leu Thr Ser Pro Asp Asp Gln Gly Val Glu Met Glu
         930   935   940

Val Phe Ser Glu Glu Asp Leu His Leu Ser Ile Gln Ser Pro Arg Lys
945   950   955   960

Lys Ser Asp Ala Val Ser Met Leu Ser Glu Cys Ser Thr Ile Asp Leu
         965   970   975

Asn Asp Ile Phe Arg Asn Leu Gln Lys Thr Val Ser Pro Lys Lys Gln
         980   985   990

Pro Asp Arg Cys Phe Pro Lys Gly Leu Ser Cys His Phe Leu Cys His

995   1000   1005

Lys Thr Asp Lys Arg Lys Ser Pro Trp Val Leu Trp Trp Asn Ile Arg
    1010   1015   1020
Lys Thr Cys Tyr Gln Ile Val Lys His Ser Trp Phe Glu Ser Phe Ile
025   1030   1035   1040

Ile Phe Val Ile Leu Leu Ser Ser Gly Ala Leu Ile Phe Glu Asp Val
            1045   1050   1055

Asn Leu Pro Ser Arg Pro Gln Val Glu Lys Leu Leu Arg Cys Thr Asp
        1060   1065   1070

Asn Ile Phe Thr Phe Ile Phe Leu Leu Glu Met Ile Leu Lys Trp Val
    1075   1080   1085

Ala Phe Gly Phe Arg Arg Tyr Phe Thr Ser Ala Trp Cys Trp Leu Asp
    1090   1095   1100

Phe Leu Ile Val Val Val Ser Val Leu Ser Leu Met Asn Leu Pro Ser
105   1110   1115   1120

Leu Lys Ser Phe Arg Thr Leu Arg Ala Leu Arg Pro Leu Arg Ala Leu
            1125   1130   1135

Ser Gln Phe Glu Gly Met Lys Val Val Val Tyr Ala Leu Ile Ser Ala
        1140   1145   1150

Ile Pro Ala Ile Leu Asn Val Leu Leu Val Cys Leu Ile Phe Trp Leu
        1155   1160   1165

Val Phe Cys Ile Leu Gly Val Asn Leu Phe Ser Gly Lys Phe Gly Arg
        1170   1175   1180

Cys Ile Asn Gly Thr Asp Ile Asn Met Tyr Leu Asp Phe Thr Glu Val
185   1190   1195   1200

Pro Asn Arg Ser Gln Cys Asn Ile Ser Asn Tyr Ser Trp Lys Val Pro
          1205   1210   1215

Gln Val Asn Phe Asp Asn Val Gly Asn Ala Tyr Leu Ala Leu Leu Gln
          1220   1225   1230

Val Ala Thr Tyr Lys Gly Trp Leu Glu Ile Met Asn Ala Ala Val Asp
          1235   1240   1245

Ser Arg Glu Lys Asp Glu Gln Pro Asp Phe Glu Ala Asn Leu Tyr Ala
          1250   1255   1260

Tyr Leu Tyr Phe Val Val Phe Ile Ile Phe Gly Ser Phe Phe Thr Leu
265   1270   1275   1280

Asn Leu Phe Ile Gly Val Ile Ile Asp Asn Phe Asn Gln Gln Gln Lys
          1285   1290   1295

Lys Leu Gly Gly Gln Asp Ile Phe Met Thr Glu Glu Gln Lys Lys Tyr
          1300   1305   1310

Tyr Asn Ala Met Lys Lys Leu Gly Thr Lys Lys Pro Gln Lys Pro Ile
          1315   1320   1325

Pro Arg Pro Leu Asn Lys Cys Gln Ala Phe Val Phe Asp Leu Val Thr
          1330   1335   1340

Ser Gln Val Phe Asp Val Ile Ile Leu Gly Leu Ile Val Leu Asn Met
345   1350   1355   1360

Ile Ile Met Met Ala Glu Ser Ala Asp Gln Pro Lys Asp Val Lys Lys
          1365   1370   1375

Thr Phe Asp Ile Leu Asn Ile Ala Phe Val Val Ile Phe Thr Ile Glu
          1380   1385   1390

Cys Leu Ile Lys Val Phe Ala Leu Arg Gln His Tyr Phe Thr Asn Gly
          1395   1400   1405

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Trp Asn Leu Phe Asp Cys Val Val Val Leu Ser Ile Ile Ser Thr
    1410             1415              1420

Leu Val Ser Arg Leu Glu Asp Ser Asp Ile Ser Phe Pro Pro Thr Leu
425             1430              1435              1440

Phe Arg Val Val Arg Leu Ala Arg Ile Gly Arg Ile Leu Arg Leu Val
            1445              1450              1455

Arg Ala Ala Arg Gly Ile Arg Thr Leu Leu Phe Ala Leu Met Met Ser
            1460              1465              1470

Leu Pro Ser Leu Phe Asn Ile Gly Leu Leu Leu Phe Leu Val Met Phe
            1475              1480              1485

Ile Tyr Ala Ile Phe Gly Met Ser Trp Phe Ser Lys Val Lys Lys Gly
    1490              1495              1500

Ser Gly Ile Asp Asp Ile Phe Asn Phe Glu Thr Phe Thr Gly Ser Met
505              1510              1515              1520

Leu Cys Leu Phe Gln Ile Thr Thr Ser Ala Gly Trp Asp Thr Leu Leu
            1525              1530              1535

Asn Pro Met Leu Glu Ala Lys Glu His Cys Asn Ser Ser Ser Gln Asp
            1540              1545              1550

Ser Cys Gln Gln Pro Gln Ile Ala Val Val Tyr Phe Val Ser Tyr Ile
    1555              1560              1565

Ile Ile Ser Phe Leu Ile Val Val Asn Met Tyr Ile Ala Val Ile Leu
    1570              1575              1580

Glu Asn Phe Asn Thr Ala Thr Glu Glu Ser Glu Asp Pro Leu Gly Glu
585              1590              1595              1600

Asp Asp Phe Glu Ile Phe Tyr Glu Val Trp Glu Lys Phe Asp Pro Glu
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1605   1610   1615

Ala Ser Gln Phe Ile Gln Tyr Ser Ala Leu Ser Asp Phe Ala Asp Ala
   1620   1625   1630

Leu Pro Glu Pro Leu Arg Val Ala Lys Pro Asn Lys Phe Gln Phe Leu
   1635   1640   1645

Val Met Asp Leu Pro Met Val Met Gly Asp Arg Leu His Cys Met Asp
   1650   1655   1660

Val Leu Phe Ala Phe Thr Thr Arg Val Leu Gly Asp Ser Ser Gly Leu
665   1670   1675   1680

Asp Thr Met Lys Thr Met Met Glu Glu Lys Phe Met Glu Ala Asn Pro
     1685   1690   1695

Phe Lys Lys Leu Tyr Glu Pro Ile Val Thr Thr Thr Lys Arg Lys Glu
     1700   1705   1710

Glu Glu Gln Gly Ala Ala Val Ile Gln Arg Ala Tyr Arg Lys His Met
     1715   1720   1725

Glu Lys Met Val Lys Leu Arg Leu Lys Asp Arg Ser Ser Ser Ser His
     1730   1735   1740

Gln Val Phe Cys Asn Gly Asp Leu Ser Ser Leu Asp Val Ala Lys Val
745   1750   1755   1760

Lys Val His Asn Asp
     1765

<210> 3

<211> 299

<212> DNA

<213> Homo sapiens

<400> 3

atcctagggc aggctgtttt attcccgcct cctgaggcct ttctgaggat ctgtggcttg 60

tctctgtcct gagggtgaag atggatgaca gatgctaccc agtaatcttt ccagatgagc 120

ggaatttccg ccccttcact tccgactctc tggctgcaat tgagaagcgg attgccatcc 180

aaaaggagaa aaagaagtct aaagaccaga caggagaagt accccagcct caacctcagc 240
ttgacctaaa ggcctccagg aagttgccca actctatggc gacaatcctc ggaggcttt 299

<210> 4

<211> 140

<212> DNA

<213> Homo sapiens

<400> 4

cgctctgtga agaagctggt caacgtgatt atcctcacct tcttttgcct cagcatcttt 60

gccctggtag gtcagcagct cttcatggga agtctgaacc tgaaatgcat ctcgagggac 120

tgtaaaaata tcagtaaccc 140

<210> 5

<211> 232

<212> DNA

<213> Homo sapiens

<400> 5

taaaaatatc agtaacccgg aagcttatga ccattgcttt gaaagaaag aaaattcacc 60

tgaattcaaa atgtgtggca tctggatggg taacagtgcc tgttccatac aatatgaatg 120

taagcacacc aaaattaatc ctgactataa ttatacgaat tttgacaact ttggctggtc 180

ttttcttgcc atgttccggc tgatgaccca agattcctgg gagaagcttt at 232

<210> 6
<211> 180
<212> DNA
<213> Homo sapiens

<400> 6
actactgggt ctactcagtc ttcttcttca ttgtggtcat tttcctgggg ctcccttcta 60
cctgattaac ttaaaccctg gctgttgtta ccatgggcat atgaggagcc gaacaagaat 120

gtagctgcag agatagaggc ccaggaaaag atgttcagga agcccagcag ctggttaaag 180

<210> 7
<211> 180
<212> DNA
<213> Homo sapiens

<400> 7
tatcactgga ccactttgat gagcatggag atcctctcca aaggcagaga gcactgagtg 60

ttgtcagcat cctcaccatc accatgaagg gtaagttcca catcccaatc caagggaaag 120

tctacttcag tgatgtcctt ccattcttct tcttcccaat cccctagaag ccctctgcaa 180

<210> 8
<211> 299
<212> DNA
<213> Homo sapiens

<400> 8
gagaaatctg gattgcctca gagctaattc ctcaacctct cgcgcattct cctccagaac 60

aagaaaaatc acaagagcct tgtctccctt gtggagaaaa cctggcatcc aagtacctcg 120

tgtggaactg ttgcccccag tggctgtgcg taaagaaggt cctgagaacc gtcatgacgg 180

tcccgtttac tgagctggac atcacgatct gcatcatcat caacacagac ttcttggaca 240

tggagcatca caagatgtaa ggcaacgtat tggagacgat gttgaatata gggcagtag 299

<210> 9
<211> 335
<212> DNA
<213> Homo sapiens

<400> 9
gcagatggag ttcgcttaac tggcttttct ccgttttcgt tcgtcgcttt ttctacagct 60

caggtcttca agtaccaaat cctggccaac tttgaacaca ctaattaaga taatccggca 120

actctcgtcg gagcccttgg aagcctgact gtggtcctgg tcattgtgat ctttattttc 180

tcagtagttg gcatgcagct ttttggccgt agcttcaatt cccaaaagag tccaaaactc 240

tgtaacccga caggcccgac agtctcatgt ttacggcact ggcacatggg ggatttctgg 300

cactccttcc tagtggtatc gcgcatcctc ttgcg 335

<210> 10
<211> 261
<212> DNA
<213> Homo sapiens

<400> 10
ctctgtacca aagaccctgg gcgtcaggca tgattggact tggttggcac cacttgcgga 60

ggaggaagat gacgttgaat tttctggtga agataatgca cagcgcatca cacaacctga 120

gcctgaacaa caggtatgaa ggttcacaca tagacttaaa ggtcatacaa agctggagtt 180

atcacagggc actggtagcc tacccttttc taggcactat gcaaggataa taaggattct 240

cgtacgcacg ggtacgattc g 261

<210> 11
<211> 215
<212> DNA
<213> Homo sapiens

<400> 11
cagacaatga gaaactccgt actactatgg tgaaagaagg tcttagtaaa aggcacccccc 60

ttccttttgt tctgatgtgc agaagtctga tgttaccagt atactatcag aatgtagcac 120

cattgatctt caggatggct ttggatggtt acctgagatg gttcccaaag aaaaatttcc 180

agcgattttt cgtaccaacg gttacgcttc gaagg 215

<210> 12
<211> 346
<212> DNA
<213> Homo sapiens

<400> 12
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agaaccttcc ggatctacga gcactgaggc ctctcgtgcg ctgtcccagt ttgaaggaat 120

gaaggtacat tctgcagaag aatgggtaga agttcagtta acagagaaag gtggaaagac 180

caacagttct ttttgggctg agatttcctt aaattgccaa gctttcctg ggttacttac 240

cagcctgccc agtgcttaga atttgagggg tagagaaaag cctaagatat actttctacc 300

ctaaaagctt ctgtgacagc caagatgagc tgtagcgaag gaattc 346

<210> 13
<211> 223
<212> DNA
<213> Homo sapiens

<400> 13
ggtgcatccc taccccatct gttatggttt cctttgctt ttgttttcca taaggtggtg 60

gtcaatgctc tcataggtgc catacctccc attcctgaat gttttgcttg tctgcctcat 120

tttctggctc gtattttgta ttctgggagt atacttcctt ttcctggaaa atttgggaaa 180

tgcattcaat ggaacagact tttaggaatt tccagcgatt cct 223

<210> 14
<211> 244
<212> DNA
<213> Homo sapiens

<400> 14
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atcgtttatg cagctgttga ttccacagag gtgagtcagt gttctaccat gttcggcagt 120

gttatggtca agtcagagat atcatgacta catggacagt ccagaactgg cgtcatagtt 180

ccagcagctg gggttctctg ccttgtttcc tttggaacaa aacactatga gataccactg 240

ccta 244

<210> 15
<211> 409
<212> DNA
<213> Homo sapiens

<400> 15

atccacccca ggccccgcca catgccatca ctccaagctg agctgcgaaa actgaaagac 60

aggctcccaa caggggctat ggctgttagg aagaggctat gtagtcaatg ttgctgctaa 120

gaaacacctt ggtcttctag ataaggtagt tagaatgctt atatttttct ccagtaattg 180

ttttttttctc ttattaaaaa aatttctaac agaaagaaca acagccagag tttgagagca 240

attcactcgg ttacatttct tcgtagtctt tatcatcttt ggctcattct tcactctgaa 300

tctcttcatt ggcgttatca ttgacaactt caaccaacag cagaaaaga taagtatctg 360

ggttgtcttg atttggtaat tgtatctctg tcctccaaag aaggaatcc 409

<210> 16
<211> 585
<212> DNA
<213> Homo sapiens

<400> 16

tttcccagac aatacaaggt ctcgtgtgcc catagcccag gcagtctttt cgacatcatc 60

ataagctcat acctaaacca tgattggctt gatggcctaa atatacaacc aaccccaaag 120

ccatggaatc catccttgac catctccaac tgggtctttg tggtcatctt tacgttagaa 180

tgtctcatca aaatctttgc tttgaggcaa tactacttca ccaatggctg gaatttattt 240

gactgtgtgg tcgtgcttct ttccattgtt agtaagtaaa atcagcagtc agagggactt 300

taagaaccag aagtaagttt gtaaatctta tcattttttg aagtttgttc aaactatcca 360

caaagcagaa aactgggcca agtgtacttt ctgaaagaat agacaggggt actaatgcca 420

ttctctactg ggaagttgct aggagatagg aggcggtaaa tttctggttc cccttaactc 480

actacacaac tgaaatagag ttcaataatc atgcagctaa tgtattcaat ggaaatagac 540

aaaattaaaa tgactcagaa gtttttgtgg tggtagaaaa atttc 585

<210> 17
<211> 223
<212> DNA
<213> Homo sapiens

<400> 17·
tgaccaaggt ggaccaaaat gacttgggaa aacgggcctc attcaccact ccagactctt 60

tgcaatggag acttgtctag ctttggggtg gccaagggca aggtccactg tgactgagcc 120

ctcacctcca cgcctacctc atagcttcac agccttgcct tcagcctctg agctccaggg 180

gtcagcagct tagtgtatca acagggagtg gattcaccaa att 223

<210> 18
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
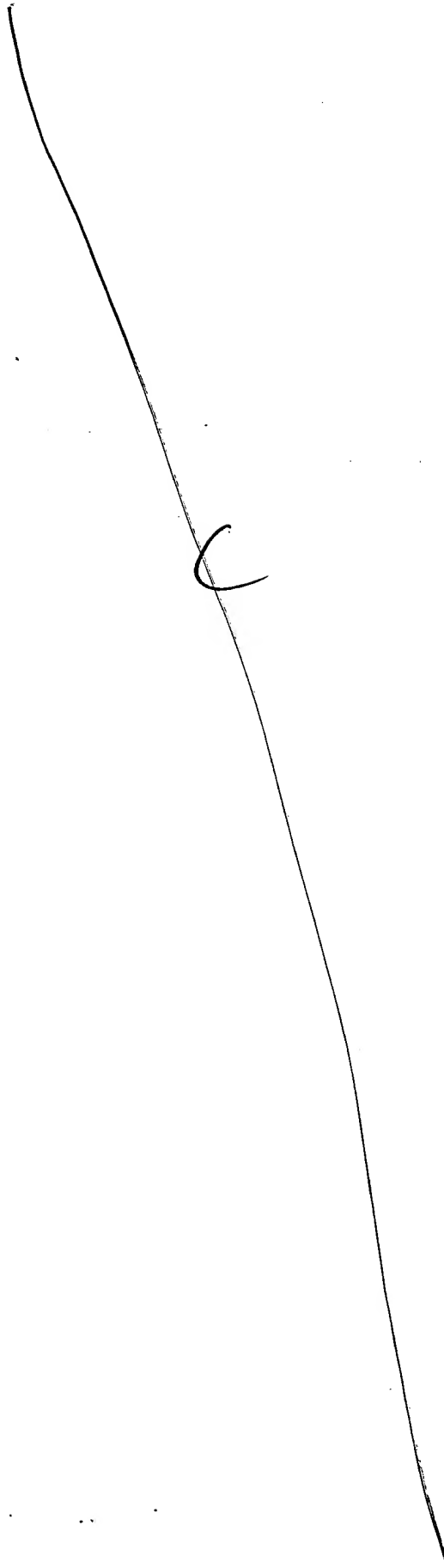<223> Description of Artificial Sequence: Primer

<400> 18
cctsgtcatg ttcatctac 19

<210> 19
<211> 22
<212> DNA
<213> Artificial Sequence

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<220>
<223> Description of Artificial Sequence: Primer


<400> 19
ctcatargar aycttggarg gg                                              22




<210> 20
<211> 21
<212> DNA
<213> Artificial Sequence


<220>
<223> Description of Artificial Sequence: Primer


<400> 20
agggaggtca ccggcctgaa m                                               21




<210> 21
<211> 21
<212> DNA
<213> Artificial Sequence


<220>
<223> Description of Artificial Sequence: Primer


<400> 21
agtggatmga gamcatgtgg g                                               21




<210> 22
<211> 18
<212> PRT
<213> Artificial Sequence
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<220>

<223> Description of Artificial Sequence: Synthetic
      sequence

<400> 22

Cys Asn Gly Asp Leu Ser Ser Leu Asp Val Ala Lys Val Lys Val His
 1   5   10   15

Asn Asp

<210> 23
<211> 15
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
      sequence

<400> 23

Glu Glu Arg Tyr Tyr Pro Val Ile Phe Pro Asp Glu Arg Asn Cys
 1   5   10   15

<210> 24
<211> 30
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 24

gatcgaattc aaggagaaaa tgtttcagga   30

<210> 25
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 25
gatcgtcgac tcatttggtc tgctcaagga   30

<210> 26·
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 26
gatcgaattc ggcggtgccc tacccacctc   30

<210> 27
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 27
gatcgtcgac tcattccatt tcaaccccctt   30

<210> 28
<211> 30
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 28

gatcgaattc aagcacaact gtggccccaa   30

<210> 29

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 29

gatcgtcgac tcacattatg aagtcttcgc   30

<210> 30

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:
      Oligonucleotide

<400> 30

agtacctctc ctccatct   18

<210> 31

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:

Oligonucleotide

<400> 31
agtactcatc cctcatct   18

<210> 32
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:.
      Oligonucleotide

<400> 32
caccgggtag tacctctc   18

<210> 33
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
      Oligonucleotide

<400> 33
cacgcgctag tcactctc   18

<210> 34
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
      Oligonucleotide

<400> 34

gtctttggac ttcttcct   18

<210> 35

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:
      Oligonucleotide

<400> 35

gtctggtgac tctttcct   18